SPECIFICATION:

Please replace the paragraph with the beginning at page 58, line 7 with the paragraph below:

1. Identification genes encoding the phagotopes. Phage clones specifically reacting with patient sera, as determined by microarray immunoscreening, can be amplified by PCR using T7 capsid forward and reverse primers. PCR fragments were purified and 100 ng of fragment was analyzed to determine the nucleotide sequence of the cDNA insets. Sequence alignments are performed using BLAST™ software **(Basic Local Alignment Search Tool (BLAST)** finds regions of local similarity between sequences, the program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches.) and GenBank™ data bases (GenBank is the NIH genetic sequence database). The sequence information can be used in several ways. Initially, the DNA sequence information provides a database of the frequency of reactivity to a particular epitope.